ABSTRACT

Heterogeneous compound databases can be searched for compounds which are likely to have the same biological activity as a known (query) molecule. Query molecules and the molecules in the database are split into fragments according to common fragmentation rules. Fragments are aligned in a uniform conformation according to a topomeric alignment process and interaction energy fields, typically steric fields, between a probe and the fragment atoms are generated to capture the fragment shapes. Comparison of the fields for the query fragments with the fields for the database compound fragments yields a measure of shape similarity. Searches for similarly shaped substructures and cores can also be readily accomplished. Pharmacophoric style features can be defined for the topomerically aligned fragments but with user specified weighting of the importance of each. Differences in features are defined with the same dimensionality as shape so that both shape and features can be used to search.

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